

# Resource Summary Report

Generated by T1D on Sep 19, 2026

## NARWHAL

RRID:SCR\_011858

Type: Tool

### Proper Citation

NARWHAL (RRID:SCR\_011858)

### Resource Information

**URL:** <https://trac.nbic.nl/narwhal/>

**Proper Citation:** NARWHAL (RRID:SCR\_011858)

**Description:** Automates the primary analysis of massive parallel sequencing data.

**Abbreviations:** NARWHAL

**Resource Type:** software resource

**Resource Name:** NARWHAL

**Resource ID:** SCR\_011858

**Alternate IDs:** OMICS\_01130

**Record Creation Time:** 20220129T080307+0000

**Record Last Update:** 20260919T195219+0000

### Ratings and Alerts

No rating or validation information has been found for NARWHAL.

No alerts have been found for NARWHAL.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

### Usage and Citation Metrics

We found 10 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

van Nistelrooij AMJ, et al. (2018) Germline variant in MSX1 identified in a Dutch family with clustering of Barrett's esophagus and esophageal adenocarcinoma. *Familial cancer*, 17(3), 435.

Silva CT, et al. (2018) A combined linkage, microarray and exome analysis suggests MAP3K11 as a candidate gene for left ventricular hypertrophy. *BMC medical genomics*, 11(1), 22.

Meuwissen ME, et al. (2016) Human USP18 deficiency underlies type 1 interferonopathy leading to severe pseudo-TORCH syndrome. *The Journal of experimental medicine*, 213(7), 1163.

Silva CT, et al. (2016) A Combined Linkage and Exome Sequencing Analysis for Electrocardiogram Parameters in the Erasmus Rucphen Family Study. *Frontiers in genetics*, 7, 190.

Demirkan A, et al. (2015) Insight in genome-wide association of metabolite quantitative traits by exome sequence analyses. *PLoS genetics*, 11(1), e1004835.

Wessel J, et al. (2015) Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature communications*, 6, 5897.

Derks KW, et al. (2015) Deciphering the RNA landscape by RNAome sequencing. *RNA biology*, 12(1), 30.

Derks KW, et al. (2015) RNAome sequencing delineates the complete RNA landscape. *Genomics data*, 5, 381.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. *Database : the journal of biological databases and curation*, 2015.

Stadhouders R, et al. (2012) Dynamic long-range chromatin interactions control Myb proto-oncogene transcription during erythroid development. *The EMBO journal*, 31(4), 986.